

#14 1652

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RAW SEQUENCE LISTING

DATE: 04/23/2002

PATENT APPLICATION: US/09/277,401A

TIME: 10:47:35

Input Set : A:\Sequence List.txt

Output Set: N:\CRF3\04232002\I277401A.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

4 (i) APPLICANT: Jaye, Michael C.

5 Lynch, Kevin J.

6 Amin, Dilip V.

7 Doan, Kim-Anh T.

8 Marchadier, Dawn

9 Maugeais, Cyrille

10 Rader, Daniel J.

11 Krawiec, John A.

12 South, Victoria J.

13 (ii) TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR EFFECTING THE
14 LEVELS OF HIGH DENSITY LIPOPROTEIN (HDL) CHOLESTEROL AND
15 APOLIPOPROTEIN AI, VERY LOW DENSITY LIPOPROTEIN
16 (VLDL) CHOLESTEROL AND LOW DENSITY LIPOPROTEIN (LDL)

CHOLESTEROL

17 (iii) NUMBER OF SEQUENCES: 31

18 (iv) CORRESPONDENCE ADDRESS:

19 (A) ADDRESSEE: Synnestvedt & Lechner LLP

20 (B) STREET: Suite 2600 Aramark Tower, 1101 Market Street

21 (C) CITY: Philadelphia

22 (D) STATE: PA

23 (E) COUNTRY: USA

24 (F) ZIP: 19107

25 (v) COMPUTER READABLE FORM:

26 (A) MEDIUM TYPE: Floppy disk

27 (B) COMPUTER: IBM PC compatible

28 (C) OPERATING SYSTEM: PC-Windows 95

29 (D) SOFTWARE: Corel WordPerfect 8.0 converted to ASCII

30 (vi) CURRENT APPLICATION DATA:

C--> 31 (A) APPLICATION NUMBER: US/09/277,401A

C--> 32 (B) FILING DATE: 26-Mar-1999

33 (C) CLASSIFICATION:

34 (viii) ATTORNEY/AGENT INFORMATION:

35 (A) NAME: Kelly, Ph.D., Patrick J.

36 (B) REGISTRATION NUMBER: 34,638

37 (C) REFERENCE/DOCKET NUMBER: 22,944-C USA

39 (ix) TELECOMMUNICATION INFORMATION:

40 (A) TELEPHONE: (215)923-4466

41 (B) TELEFAX: (215)923-2189

43 (2) INFORMATION FOR SEQ ID NO: 1:

44 (i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 367 base pairs

46 (B) TYPE: nucleic acid

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47          (C) STRANDEDNESS: double
48          (D) TOPOLOGY: linear
49      (ii) MOLECULE TYPE: cDNA
50      (ix) FEATURE:
51          (A) NAME/KEY: CDS
52          (B) LOCATION: 22..180
53      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
54 GAATTCGGCT TGATCAATCG C TTC AAA AAG GGG ATC TGT CTG AGC TGC CGC      51
55          Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg
56          1          5          10
57 AAG AAC CGT TGT AAT AGC ATT GGC TAC AAT GCC AAG AAA ATG AGG AAC      99
58 Lys Asn Arg Cys Asn Ser Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn
59          15          20          25
62 AAG AGG AAC AGC AAA ATG TAC CTA AAA ACC CGG GCA GGC ATG CCT TTC      147
63 Lys Arg Asn Ser Lys Met Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe
64          30          35          40
65 AGA GGT AAC CTT CAG TCC CTG GAG TGT CCC TGA GGAAGGCCCT TAATACCTCC      200
66 Arg Gly Asn Leu Gln Ser Leu Glu Cys Pro
67          45          50
68 TTCTTAATAC CATGCTGCAG AGCAGGGCAC ATCCTAGCCC AGGAGAAGTG GCCAGCACAA      260
69 TCCAATCAAAA TCGTTGCAAA TCAGATTACA CTGTGCATGT CCTAGGAAAAG GGAATCTTTA      320
70 CAAAATAAAC AGTGTGGACC CCTCAAAAAA AAAAAAAGC CGAATTC      367
72 (2) INFORMATION FOR SEQ ID NO: 2:
73      (i) SEQUENCE CHARACTERISTICS:
74          (A) LENGTH: 52 amino acids
75          (B) TYPE: amino acid
76          (D) TOPOLOGY: linear
77      (ii) MOLECULE TYPE: protein
78      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
79 Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg Cys Asn Ser
80 1          5          10          15
81 Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg Asn Ser Lys Met
82          20          25          30
83 Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe Arg Gly Asn Leu Gln Ser
84          35          40          45
85 Leu Glu Cys Pro
86          50
88 (2) INFORMATION FOR SEQ ID NO: 3:
89      (i) SEQUENCE CHARACTERISTICS:
90          (A) LENGTH: 1382 base pairs
91          (B) TYPE: nucleic acid
92          (C) STRANDEDNESS: double
93          (D) TOPOLOGY: linear
94      (ii) MOLECULE TYPE: cDNA
95      (ix) FEATURE:
96          (A) NAME/KEY: CDS
97          (B) LOCATION: 312..1370
98      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
99 GAATTCGGCT TCTACTACTA CTAGGCCACG CGTCGCCTAG TACGGGGGGG GGGGGGGGGG      60

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100	TCAGCGAGTC	CTTGCCCTCCC	GGCGGCTCAG	GACGAGGGCA	GATCTCGTTC	TGGGGCAAGC	120
101	CGTTGACACT	CGCTCCCTGC	CACCGCCCCG	GCTCCGTGCC	GCCAAGTTTT	CATTTTCCAC	180
102	CTTCTCTGCC	TCCAGTCCCC	CAGCCCCTGG	CCGAGAGAAG	GGTCTTACCG	GCCGGGATTG	240
103	CTGGAAACAC	CAAGAGGTGG	TTTTTGTTTT	TTAAAACTTC	TGTTTCTTGG	GAGGGGGTGT	300
104	GGCGGGGCAG	G	ATG	AGC	AAC	TCC	350
105		Met	Ser	Asn	Ser	Val	
106		1			5		
107	TGC	TAT	TGC	TTT	GCT	GCG	398
108	Cys	Tyr	Cys	Phe	Ala	Ala	
109	15				20		
110	CGG	CTG	GAA	GAT	AAG	CTC	446
111	Arg	Leu	Glu	Asp	Lys	Leu	
112	30				35		
113	AAA	CCA	TCT	GTG	AGG	TTT	494
114	Lys	Pro	Ser	Val	Arg	Phe	
115					50		
116	GAA	GGA	TGC	TAC	CTC	TCC	542
117	Glu	Gly	Cys	Tyr	Leu	Ser	
118					65		
119	AGT	TTC	AAC	ATG	ACA	GCT	590
120	Ser	Phe	Asn	Met	Thr	Ala	
121					80		
123	ATG	AGC	GGT	ATC	TTT	GAA	638
124	Met	Ser	Gly	Ile	Phe	Glu	
125					95		
126	CAC	ACA	AGA	GAG	AAA	GAC	686
127	His	Thr	Arg	Glu	Lys	Asp	
128	110				115		
129	CTG	GCC	CAC	CAG	CTT	TAC	734
130	Leu	Ala	His	Gln	Leu	Tyr	
131					130		
132	GGA	CAC	AGC	ATT	GCC	AGG	782
133	Gly	His	Ser	Ile	Ala	Arg	
134					145		
135	TTT	TCT	CTC	GGG	AAT	GTC	830
136	Phe	Ser	Leu	Gly	Asn	Val	
137					160		
138	GTG	GCC	GGG	TAT	GCA	GGC	878
139	Val	Ala	Gly	Tyr	Ala	Gly	
140					175		
141	ACA	GGT	TTG	GAT	CCT	GCC	926
142	Thr	Gly	Leu	Asp	Pro	Ala	
143	190				195		
144	AAG	AGG	CTC	TCT	CCG	GAC	974
145	Lys	Arg	Leu	Ser	Pro	Asp	
146					210		
147	TAC	ACG	CGT	TCC	TTC	GGC	1022
148	Tyr	Thr	Arg	Ser	Phe	Gly	
149					225		

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150 CAC ATT GAC ATC TAC CCC AAT GGG GGT GAC TTC CAG CCA GGC TGT GGA      1070
151 His Ile Asp Ile Tyr Pro Asn Gly Gly Asp Phe Gln Pro Gly Cys Gly
152      240      245      250
153 CTC AAC GAT GTC TTG GGA TCA ATT GCA TAT GGA ACA ATC ACA GAG GTG      1118
154 Leu Asn Asp Val Leu Gly Ser Ile Ala Tyr Gly Thr Ile Thr Glu Val
155      255      260      265
156 GTA AAA TGT GAG CAT GAG CGA GCC GTC CAC CTC TTT GTT GAC TCT CTG      1166
157 Val Lys Cys Glu His Glu Arg Ala Val His Leu Phe Val Asp Ser Leu
158 270      275      280      285
159 GTG AAT CAG GAC AAG CCG AGT TTT GCC TTC CAG TGC ACT GAC TCC AAT      1214
160 Val Asn Gln Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser Asn
161      290      295      300
162 CGC TTC AAA AAG GGG ATC TGT CTG AGC TGC CGC AAG AAC CGT TGT AAT      1262
163 Arg Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg Cys Asn
164      305      310      315
165 AGC ATT GGC TAC AAT GCC AAG AAA ATG AGG AAC AAG AGG AAC AGC AAA      1310
166 Ser Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg Asn Ser Lys
167      320      325      330
168 ATG TAC CTA AAA ACC CGG GCA GGC ATG CCT TTC AGA GGT AAC CTT CAG      1358
169 Met Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe Arg Gly Asn Leu Gln
170      335      340      345
171 TCC CTG GAG TGT CAAGCCGAAT TC      1382
172 Ser Leu Glu Cys
173 350
175 (2) INFORMATION FOR SEQ ID NO: 4:
176 (i) SEQUENCE CHARACTERISTICS:
177 (A) LENGTH: 353 amino acids
178 (B) TYPE: amino acid
179 (D) TOPOLOGY: linear
180 (ii) MOLECULE TYPE: protein
181 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
182 Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu Cys Tyr Cys
183 1      5      10      15
184 Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly Arg Leu Glu
185      20      25      30
186 Asp Lys Leu His Lys Pro Lys Ala Thr Gln Thr Glu Val Lys Pro Ser
187      35      40      45
188 Val Arg Phe Asn Leu Arg Thr Ser Lys Asp Pro Glu His Glu Gly Cys
189      50      55      60
190 Tyr Leu Ser Val Gly His Ser Gln Pro Leu Glu Asp Cys Ser Phe Asn
191 65      70      75      80
192 Met Thr Ala Lys Thr Phe Phe Ile Ile His Gly Trp Thr Met Ser Gly
193      85      90      95
194 Ile Phe Glu Asn Trp Leu His Lys Leu Val Ser Ala Leu His Thr Arg
195      100      105      110
196 Glu Lys Asp Ala Asn Val Val Val Asp Trp Leu Pro Leu Ala His
197      115      120      125
198 Gln Leu Tyr Thr Asp Ala Val Asn Asn Thr Arg Val Val Gly His Ser
199      130      135      140

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```

200 Ile Ala Arg Met Leu Asp Trp Leu Gln Glu Lys Asp Asp Phe Ser Leu
201 145                      150                      155                      160
202 Gly Asn Val His Leu Ile Gly Tyr Ser Leu Gly Ala His Val Ala Gly
203                      165                      170                      175
204 Tyr Ala Gly Asn Phe Val Lys Gly Thr Val Gly Arg Ile Thr Gly Leu
205                      180                      185                      190
206 Asp Pro Ala Gly Pro Met Phe Glu Gly Ala Asp Ile His Lys Arg Leu
207                      195                      200                      205
208 Ser Pro Asp Asp Ala Asp Phe Val Asp Val Leu His Thr Tyr Thr Arg
209                      210                      215                      220
210 Ser Phe Gly Leu Ser Ile Gly Ile Gln Met Pro Val Gly His Ile Asp
211 225                      230                      235                      240
212 Ile Tyr Pro Asn Gly Gly Asp Phe Gln Pro Gly Cys Gly Leu Asn Asp
213                      245                      250                      255
214 Val Leu Gly Ser Ile Ala Tyr Gly Thr Ile Thr Glu Val Val Lys Cys
215                      260                      265                      270
216 Glu His Glu Arg Ala Val His Leu Phe Val Asp Ser Leu Val Asn Gln
217                      275                      280                      285
218 Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser Asn Arg Phe Lys
219                      290                      295                      300
220 Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg Cys Asn Ser Ile Gly
221 305                      310                      315                      320
222 Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg Asn Ser Lys Met Tyr Leu
223                      325                      330                      335
224 Lys Thr Arg Ala Gly Met Pro Phe Arg Gly Asn Leu Gln Ser Leu Glu
225                      340                      345                      350
226 Cys

```

228 (2) INFORMATION FOR SEQ ID NO: 5:

229 (i) SEQUENCE CHARACTERISTICS:

230 (A) LENGTH: 1065 base pairs

231 (B) TYPE: nucleic acid

232 (C) STRANDEDNESS: double

233 (D) TOPOLOGY: linear

234 (ii) MOLECULE TYPE: cDNA

235 (ix) FEATURE:

236 (A) NAME/KEY: CDS

237 (B) LOCATION: 1..1065

238 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```

240 ATG AGC AAC TCC GTT CCT CTG CTC TGT TTC TGG AGC CTC TGC TAT TGC      48
241 Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu Cys Tyr Cys
242 1                      5                      10                      15
245 TTT GCT GCG GGG AGC CCC GTA CCT TTT GGT CCA GAG GGA CGG CTG GAA      96
246 Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly Arg Leu Glu
247                      20                      25                      30
248 GAT AAG CTC CAC AAA CCC AAA GCT ACA CAG ACT GAG GTC AAA CCA TCT      144
249 Asp Lys Leu His Lys Pro Lys Ala Thr Gln Thr Glu Val Lys Pro Ser
250                      35                      40                      45
251 GTG AGG TTT AAC CTC CGC ACC TCC AAG GAC CCA GAG CAT GAA GGA TGC      192
252 Val Arg Phe Asn Leu Arg Thr Ser Lys Asp Pro Glu His Glu Gly Cys

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VERIFICATION SUMMARY

DATE: 04/23/2002

PATENT APPLICATION: US/09/277,401A

TIME: 10:47:36

Input Set : A:\Sequence List.txt

Output Set: N:\CRF3\04232002\I277401A.raw

L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]